

COPY OF PAPER
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SEQUENCE LISTING

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Corixa Corporation

<120> Methods of Using a Mycobacterium tuberculosis Coding
Sequence to Facilitate Stable and High Yield Expression
of Heterologous Proteins

<130> 014058-008010US

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<160> 22

<170> PatentIn Ver. 2.1

<210> 1

<211> 1872

<212> DNA

<213> Mycobacterium tuberculosis

<220>

<223> 32 KD serine protease MTB32A

<220>

<221> CDS

<222> (89)..(1156)

<223> MTB32A

<220>

<221> sig_peptide

<222> (89)..(184)

<223> N-terminal hydrophobic secretory signal sequence

<220>

<221> mat_peptide

<222> (185)..(1153)

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Met Ser Asn Ser Arg Arg Arg Ser

-30

-25

ctc agg tgg tca tgg ttg ctg agc gtg ctg gct gcc gtc ggg ctg ggc 160

Leu Arg Trp Ser Trp Leu Leu Ser Val Leu Ala Ala Val Gly Leu Gly

-20

-15

-10

ctg gcc acg gcg ccg gcc cag gcg gcc ccg ccg gcc ttg tcg cag gac 208

Leu Ala Thr Ala Pro Ala Gln Ala Ala Pro Pro Ala Leu Ser Gln Asp

-5

-1 1

5

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cgg ttc gcc gac ttc ccc gcg ctg ccc ctc gac ccg tcc gcg atg gtc 256
 Arg Phe Ala Asp Phe Pro Ala Leu Pro Leu Asp Pro Ser Ala Met Val
 10 15 20

gcc caa gtg ggg cca cag gtg gtc aac atc aac acc aaa ctg ggc tac 304
 Ala Gln Val Gly Pro Gln Val Val Asn Ile Asn Thr Lys Leu Gly Tyr
 25 30 35 40

aac aac gcc gtg ggc gcc ggg acc ggc atc gtc atc gat ccc aac ggt 352
 Asn Asn Ala Val Gly Ala Gly Thr Gly Ile Val Ile Asp Pro Asn Gly
 45 50 55

gtc gtg ctg acc aac aac cac gtg atc gcg ggc gcc acc gac atc aat 400
 Val Val Leu Thr Asn Asn His Val Ile Ala Gly Ala Thr Asp Ile Asn
 60 65 70

gcg ttc agc gtc ggc tcc ggc caa acc tac ggc gtc gat gtg gtc ggg 448
 Ala Phe Ser Val Gly Ser Gly Gln Thr Tyr Gly Val Asp Val Val Gly
 75 80 85

tat gac cgc acc cag gat gtc gcg gtg ctg cag ctg cgc ggt gcc ggt 496
 Tyr Asp Arg Thr Gln Asp Val Ala Val Leu Gln Leu Arg Gly Ala Gly
 90 95 100

ggc ctg ccg tcg gcg gcg atc ggt ggc ggc gtc gcg gtt ggt gag ccc 544
 Gly Leu Pro Ser Ala Ala Ile Gly Gly Gly Val Ala Val Gly Glu Pro
 105 110 115 120

gtc gtc gcg atg ggc aac agc ggt ggg cag ggc gga acg ccc cgt gcg 592
 Val Val Ala Met Gly Asn Ser Gly Gly Gln Gly Gly Thr Pro Arg Ala
 125 130 135

gtg cct ggc agg gtg gtc gcg ctc ggc caa acc gtg cag gcg tcg gat 640
 Val Pro Gly Arg Val Val Ala Leu Gly Gln Thr Val Gln Ala Ser Asp
 140 145 150

tcg ctg acc ggt gcc gaa gag aca ttg aac ggg ttg atc cag ttc gat 688
 Ser Leu Thr Gly Ala Glu Glu Thr Leu Asn Gly Leu Ile Gln Phe Asp
 155 160 165

gcc gcg atc cag ccc ggt gat tcg ggc ggg ccc gtc gtc aac ggc cta 736
 Ala Ala Ile Gln Pro Gly Asp Ser Gly Gly Pro Val Val Asn Gly Leu
 170 175 180

gga cag gtg gtc ggt atg aac acg gcc gcg tcc gat aac ttc cag ctg 784
 Gly Gln Val Val Gly Met Asn Thr Ala Ala Ser Asp Asn Phe Gln Leu
 185 190 195 200

tcc cag ggt ggg cag gga ttc gcc att ccg atc ggg cag gcg atg gcg 832
 Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
 205 210 215

atc gcg ggc cag atc cga tcg ggt ggg ggg tca ccc acc gtt cat atc 880
 Ile Ala Gly Gln Ile Arg Ser Gly Gly Gly Ser Pro Thr Val His Ile
 220 225 230

ggg cct acc gcc ttc ctc ggc ttg ggt gtt gtc gac aac aac ggc aac 928
 Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn
 235 240 245

ggc gca cga gtc caa cgc gtg gtc ggg agc gct ccg gcg gca agt ctc 976
 Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu
 250 255 260

ggc atc tcc acc ggc gac gtg atc acc gcg gtc gac ggc gct ccg atc 1024
 Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile
 265 270 275 280

aac tgc gcc acc gcg atg gcg gac gcg ctt aac ggc cat cat ccc ggt 1072
 Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly
 285 290 295

gac gtc atc tgc gtg acc tgg caa acc aag tgc ggc ggc acg cgt aca 1120
 Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr
 300 305 310

ggg aac gtg aca ttg gcc gag gga ccc ccg gcc tga ttctgtcgcg 1166
 Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala
 315 320

gataccaccc gccggccggc caattggatt ggcgccagcc gtgattgccg cgtgagcccc 1226

cgagttccgt ctcccggtgcg cgtggcatcg tggaagcaat gaacgaggca gaacacagcg 1286

tcgagcaccc tcccggtgcg ggcagtcacg tcgaaggcgg tgtggtcgag catccggatg 1346

ccaaggactt cggcagcgcc gccgccctgc ccgccgatcc gacctgggtt aagcacgcgcg 1406

tcttctacga ggtgctggtc cgggcgttct tcgacgccag cgcggacggt tccggcgatc 1466

tgcgtggact catcgatcgc ctcgactacc tgcagtggct tggcatcgac tgcattcggg 1526

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acaccagcga gcgctacacc gacgcccgga tcattctcgt cgacaccgaa gagtcgaact 1826

ggtcattcga tctgtccgc cgacagttct actggcaccg attctt 1872

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<211> 355

<212> PRT

<213> Mycobacterium tuberculosis

<223> 32 KD serine protease MTB32A

<400> 2

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 20 25 30

Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala Leu
 35 40 45

Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Gly Pro Gln Val Val
 50 55 60

Asn Ile Asn/(Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly Thr
 65 70 75 80
 Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val
 85 90 95
 Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln
 100 105 110
 Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala
 115 120 125
 Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly
 130 135 140
 Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly
 145 150 155 160
 Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu
 165 170 175
 Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu Thr
 180 185 190
 Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser
 195 200 205
 Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn Thr
 210 215 220
 Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe Ala
 225 230 235 240
 Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser Gly
 245 250 255
 Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly Leu
 260 265 270
 Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val Val
 275 280 285
 Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val Ile
 290 295 300
 Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala Asp
 305 310 315 320
 Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Thr Trp Gln
 325 330 335
 Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu Gly
 340 345 350
 Pro Pro Ala
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<210> 3
 <211> 396
 <212> DNA
 <213> Mycobacterium tuberculosis

<220>
 <223> 14 KD C-terminal fragment of MTB32A Ra12

<220>
 <221> CDS
 <222> (1)..(396)
 <223> Ra12

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 Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe
 1 5 10 15
 gcc att ccg atc ggg cag gcg atg gcg atc gcg ggc cag atc cga tcg 96
 Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser
 20 25 30

ggt ggg ggg tca ccc acc gtt cat atc ggg cct acc gcc ttc ctc ggc 144
 Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly
 35 40 45
 ttg ggt gtt gtc gac aac aac ggc aac ggc gca cga gtc caa cgc gtg 192
 Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val
 50 55 60
 gtc ggg agc gct ccg gcg gca agt ctc ggc atc tcc acc ggc gac gtg 240
 Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
 65 70 75 80
 atc acc gcg gtc gac ggc gct ccg atc aac tcg gcc acc gcg atg gcg 288
 Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
 85 90 95
 gac gcg ctt aac ggg cat cat ccc ggt gac gtc atc tcg gtg acc tgg 336
 Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Thr Trp
 100 105 110
 caa acc aag tcg ggc ggc acg cgt aca ggg aac gtg aca ttg gcc gag 384
 Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu
 115 120 125
 gga ccc ccg gcc 396
 Gly Pro Pro Ala
 130

<210> 4
 <211> 132
 <212> PRT
 <213> Mycobacterium tuberculosis
 <223> 14 KD C-terminal fragment of MTB32A Ra12

<400> 4
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 Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly
 35 40 45
 Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val
 50 55 60
 Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
 65 70 75 80
 Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
 85 90 95
 Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Thr Trp
 100 105 110
 Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu
 115 120 125
 (Gly Pro Pro Ala)
 130

<210> 5
 <211> 702
 <212> DNA
 <213> Artificial Sequence

ccc ctc ccc ggc ccg ccg cca ccg ggt ggt tgc ggt ggg gca att ccg 672
 Pro Leu Pro Gly Pro Pro Pro Pro Gly Gly Cys Gly Gly Ala Ile Pro
 210 215 220

tcc gag cag ccc aac gct ccc tga gaattc 702
 Ser Glu Gln Pro Asn Ala Pro
 225 230

<210> 6
 <211> 230
 <212> PRT
 <213> Artificial Sequence
 <223> Description of Artificial Sequence:Ra12-DPPD fusion
 polypeptide

<400> 6
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 1 5 10 15
 Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
 20 25 30
 Ile Ala Gly Gln Ile Arg Ser Gly Gly Ser Pro Thr Val His Ile
 35 40 45
 Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn
 50 55 60
 Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu
 65 70 75 80
 Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile
 85 90 95
 Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly
 100 105 110
 Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr
 115 120 125
 Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala Glu Phe Asp Asp Asp
 130 135 140
 Asp Lys Asp Pro Pro Asp Pro His Gln Pro Asp Met Thr Lys Gly Tyr
 145 150 155 160
 Cys Pro Gly Gly Arg Trp Gly Phe Gly Asp Leu Ala Val Cys Asp Gly
 165 170 175
 Glu Lys Tyr Pro Asp Gly Ser Phe Trp His Gln Trp Met Gln Thr Trp
 180 185 190
 Phe Thr Gly Pro Gln Phe Tyr Phe Asp Cys Val Ser Gly Gly Glu Pro
 195 200 205
 Leu Pro Gly Pro Pro Pro Pro Gly Gly Cys Gly Gly Ala Ile Pro Ser
 210 215 220
 Glu Gln Pro Asn Ala Pro
 225 230

<210> 7
 <211> 1746
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence:Ra12-WT1 fusion
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 <222> (4)...(1740)
 <223> Ra12-WT1 fusion polypeptide

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240 245 250 255	
tgt cgc tac ggg ccc ttc ggt cct cct ccg ccc agc cag gcg tca tcc	816
Cys Arg Tyr Gly Pro Phe Gly Pro Pro Pro Ser Gln Ala Ser Ser	
260 265 270	
ggc cag gcc agg atg ttt cct aac gcg ccc tac ctg ccc agc tgc ctc	864
Gly Gln Ala Arg Met Phe Pro Asn Ala Pro Tyr Leu Pro Ser Cys Leu	
275 280 285	
gag agc cag ccc gct att cgc aat cag ggt tac agc acg gtc acc ttc	912
Glu Ser Gln Pro Ala Ile Arg Asn Gln Gly Tyr Ser Thr Val Thr Phe	
290 295 300	
gac ggg acg ccc agc tac ggt cac acg ccc tcg cac cat gcg gcg cag	960
Asp Gly Thr Pro Ser Tyr Gly His Thr Pro Ser His His Ala Ala Gln	
305 310 315	
ttc ccc aac cac tca ttc aag cat gag gat ccc atg ggc cag cag ggc	1008
Phe Pro Asn His Ser Phe Lys His Glu Asp Pro Met Gly Gln Gln Gly	
320 325 330 335	
tcg ctg ggt gag cag cag tac tcg gtg ccg ccc ccg gtc tat ggc tgc	1056
Ser Leu Gly Gln Gln Tyr Ser Val Pro Pro Pro Val Tyr Gly Cys	
340 345 350	
cac acc ccc acc gac agc tgc acc ggc agc cag gct ttg ctg ctg agg	1104
His Thr Pro Thr Asp Ser Cys Thr Gly Ser Gln Ala Leu Leu Leu Arg	
355 360 365	
acg ccc tac agc agt gac aat tta tac caa atg aca tcc cag ctt gaa	1152
Thr Pro Tyr Ser Ser Asp Asn Leu Tyr Gln Met Thr Ser Gln Leu Glu	
370 375 380	
tgc atg acc tgg aat cag atg aac tta gga gcc acc tta aag ggc cac	1200
Cys Met Thr Trp Asn Gln Met Asn Leu Gly Ala Thr Leu Lys Gly His	
385 390 395	
agc aca ggg tac gag agc gat aac cac aca acg ccc atc ctc tgc gga	1248
Ser Thr Gly Tyr Glu Ser Asp Asn His Thr Thr Pro Ile Leu Cys Gly	
400 405 410 415	
gcc caa tac aga ata cac acg cac ggt gtc ttc aga ggc att cag gat	1296
Ala Gln Tyr Arg Ile His Thr His Gly Val Phe Arg Gly Ile Gln Asp	
420 425 430	
gtg cga cgt gtg cct gga gta gcc ccg act ctt gta cgg tcg gca tct	1344
Val Arg Arg Val Pro Gly Val Ala Pro Thr Leu Val Arg Ser Ala Ser	
435 440 445	
gag acc agt gag aaa cgc ccc ttc atg tgt gct tac tca ggc tgc aat	1392
Glu Thr Ser Glu Lys Arg Pro Phe Met Cys Ala Tyr Ser Gly Cys Asn	
450 455 460	
aag aga tat ttt aag ctg tcc cac tta cag atg cac agc agg aag cac	1440
Lys Arg Tyr Phe Lys Leu Ser His Leu Gln Met His Ser Arg Lys His	
465 470 475	

act ggt gag aaa cca tac cag tgt gac ttc aag gac tgt gaa cga agg 1488
 Thr Gly Glu Lys Pro Tyr Gln Cys Asp Phe Lys Asp Cys Glu Arg Arg
 480 485 490 495

ttt ttt cgt tca gac cag ctc aaa aga cac caa agg aga cat aca ggt 1536
 Phe Phe Arg Ser Asp Gln Leu Lys Arg His Gln Arg Arg His Thr Gly
 500 505 510

gtg aaa cca ttc cag tgt aaa act tgt cag cga aag ttc tcc cgg tcc 1584
 Val Lys Pro Phe Gln Cys Lys Thr Cys Gln Arg Lys Phe Ser Arg Ser
 515 520 525

gac cac ctg aag acc cac acc agg act cat aca ggt gaa aag ccc ttc 1632
 Asp His Leu Lys Thr His Thr Arg Thr His Thr Gly Glu Lys Pro Phe
 530 535 540

agc tgt cgg tgg cca agt tgt cag aaa aag ttt gcc cgg tca gat gaa 1680
 Ser Cys Arg Trp Pro Ser Cys Gln Lys Lys Phe Ala Arg Ser Asp Glu
 545 550 555

tta gtc cgc cat cac aac atg cat cag aga aac atg acc aaa ctc cag 1728
 Leu Val Arg His His Asn Met His Gln Arg Asn Met Thr Lys Leu Gln
 560 565 570 575

ctg gcg ctt tga gaattc 1746
 Leu Ala Leu

<210> 8

<211> 578

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: Ral2-WT1 fusion
 polypeptide

<400> 8

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 20 25 30
 Ile Ala Gly Gln Ile Arg Ser Gly Gly Gly Ser Pro Thr Val His Ile
 35 40 45
 Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn
 50 55 60
 Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu
 65 70 75 80
 Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile
 85 90 95
 Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly
 100 105 110
 Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr
 115 120 125
 Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala Glu Phe Pro Leu Val
 130 135 140
 Pro Arg Gly Ser Pro Met Gly Ser Asp Val Arg Asp Leu Asn Ala Leu
 145 150 155 160
 Leu Pro Ala Val Pro Ser Leu Gly Gly Gly Gly Cys Ala Leu Pro
 165 170 175
 Val Ser Gly Ala Ala Gln Trp Ala Pro Val Leu Asp Phe Ala Pro Pro
 180 185 190

Gly Ala Ser Ala Tyr Gly Ser Leu Gly Gly Pro Ala Pro Pro Pro Ala
 195 200 205
 Pro Pro Pro Pro Pro Pro Pro His Ser Phe Ile Lys Gln Glu
 210 215 220
 Pro Ser Trp Gly Gly Ala Glu Pro His Glu Glu Gln Cys Leu Ser Ala
 225 230 235 240
 Phe Thr Val His Phe Ser Gly Gln Phe Thr Gly Thr Ala Gly Ala Cys
 245 250 255
 Arg Tyr Gly Pro Phe Gly Pro Pro Pro Ser Gln Ala Ser Ser Gly
 260 265 270
 Gln Ala Arg Met Phe Pro Asn Ala Pro Tyr Leu Pro Ser Cys Leu Glu
 275 280 285
 Ser Gln Pro Ala Ile Arg Asn Gln Gly Tyr Ser Thr Val Thr Phe Asp
 290 295 300
 Gly Thr Pro Ser Tyr Gly His Thr Pro Ser His His Ala Ala Gln Phe
 305 310 315 320
 Pro Asn His Ser Phe Lys His Glu Asp Pro Met Gly Gln Gln Gly Ser
 325 330 335
 Leu Gly Glu Gln Gln Tyr Ser Val Pro Pro Val Tyr Gly Cys His
 340 345 350
 Thr Pro Thr Asp Ser Cys Thr Gly Ser Gln Ala Leu Leu Leu Arg Thr
 355 360 365
 Pro Tyr Ser Ser Asp Asn Leu Tyr Gln Met Thr Ser Gln Leu Glu Cys
 370 375 380
 Met Thr Trp Asn Gln Met Asn Leu Gly Ala Thr Leu Lys Gly His Ser
 385 390 395 400
 Thr Gly Tyr Glu Ser Asp Asn His Thr Thr Pro Ile Leu Cys Gly Ala
 405 410 415
 Gln Tyr Arg Ile His Thr His Gly Val Phe Arg Gly Ile Gln Asp Val
 420 425 430
 Arg Arg Val Pro Gly Val Ala Pro Thr Leu Val Arg Ser Ala Ser Glu
 435 440 445
 Thr Ser Glu Lys Arg Pro Phe Met Cys Ala Tyr Ser Gly Cys Asn Lys
 450 455 460
 Arg Tyr Phe Lys Leu Ser His Leu Gln Met His Ser Arg Lys His Thr
 465 470 475 480
 Gly Glu Lys Pro Tyr Gln Cys Asp Phe Lys Asp Cys Glu Arg Arg Phe
 485 490 495
 Phe Arg Ser Asp Gln Leu Lys Arg His Gln Arg Arg His Thr Gly Val
 500 505 510
 Lys Pro Phe Gln Cys Lys Thr Cys Gln Arg Lys Phe Ser Arg Ser Asp
 515 520 525
 His Leu Lys Thr His Thr Arg Thr His Thr Gly Glu Lys Pro Phe Ser
 530 535 540
 Cys Arg Trp Pro Ser Cys Gln Lys Lys Phe Ala Arg Ser Asp Glu Leu
 545 550 555 560
 Val Arg His His Asn Met His Gln Arg Asn Met Thr Lys Leu Gln Leu
 565 570 575
 Ala Leu

<210> 9

<211> 672

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ra12-human mammaglobin fusion

<210> 10
 <211> 220
 <212> PRT
 <213> Artificial Sequence
 <223> Description of Artificial Sequence:Ra12-human mammaglobin fusion polypeptide

<400> 10
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 20 25 30
 Ile Ala Gly Gln Ile Arg Ser Gly Gly Gly Ser Pro Thr Val His Ile
 35 40 45
 Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn
 50 55 60
 Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu
 65 70 75 80
 Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile
 85 90 95
 Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly
 100 105 110
 Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr
 115 120 125
 Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala Glu Phe Ile Glu Gly
 130 135 140
 Arg Gly Ser Gly Cys Pro Leu Leu Glu Asn Val Ile Ser Lys Thr Ile
 145 150 155 160
 Asn Pro Gln Val Ser Lys Thr Glu Tyr Lys Glu Leu Leu Gln Glu Phe
 165 170 175
 Ile Asp Asp Asn Ala Thr Thr Asn Ala Ile Asp Glu Leu Lys Glu Cys
 180 185 190
 Phe Leu Asn Gln Thr Asp Glu Thr Leu Ser Asn Val Glu Val Phe Met
 195 200 205
 Gln Leu Ile Tyr Asp Ser Ser Leu Cys Asp Leu Phe
 210 215 220

<210> 11
 <211> 2191
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Ra12-H9-32A fusion
 (Ra12-MTB39-MTB32A(N-ter) fusion)

<220>
 <221> CDS
 <222> (1)..(2190)
 <223> Ra12-H9-32A (Ra12-MTB39-MTB32A(N-ter)) fusion polypeptide

<400> 11
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 Met His His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu
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 tcc cag ggt ggg cag gga ttc gcc att ccg atc ggg cag gcg atg gcg 96
 Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
 20 25 30

atc gcg ggc cag atc cga tgc ggt ggg ggg tca ccc acc gtt cat atc	144
Ile Ala Gly Gln Ile Arg Ser Gly Gly Ser Pro Thr Val His Ile	
35 40 45	
ggg cct acc gcc ttc ctc ggc ttg ggt gtt gtc gac aac aac ggc aac	192
Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn	
50 55 60	
ggc gca cga gtc caa cgc gtg gtc ggg agc gct ccg gcg gca agt ctc	240
Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu	
65 70 75 80	
ggc atc tcc acc ggc gac gtg atc acc gcg gtc gac ggc gct ccg atc	288
Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile	
85 90 95	
aac tgc gcc acc gcg atg gcg gac gcg ctt aac ggg cat cat ccc ggt	336
Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly	
100 105 110	
gac gtc atc tgc gtg acc tgg caa acc aag tgc ggc ggc acg cgt aca	384
Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr	
115 120 125	
ggg aac gtg aca ttg gcc gag gga ccc ccg gcc gaa ttc atg gtg gat	432
Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala Glu Phe Met Val Asp	
130 135 140	
ttc ggg gcg tta cca ccg gag atc aac tcc gcg agg atg tac gcc ggc	480
Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly	
145 150 155 160	
ccg ggt tgc gcc tgc ctg gtg gcc gcg gct cag atg tgg gac agc gtg	528
Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Gln Met Trp Asp Ser Val	
165 170 175	
gcg agt gac ctg ttt tgc gcc gcg tgc gcg ttt cag tgc gtg gtc tgg	576
Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser Val Val Trp	
180 185 190	
ggt ctg acg gtg ggg tgc tgg ata ggt tgc tgc gcg ggt ctg atg gtg	624
Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly Leu Met Val	
195 200 205	
gcg gcg gcc tgc ccg tat gtg gcg tgg atg agc gtc acc gcg ggg cag	672
Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr Ala Gly Gln	
210 215 220	
gcc gag ctg acc gcc gcc cag gtc cgg gtt gct gcg gcg gcc tac gag	720
Ala Glu Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala Ala Tyr Glu	
225 230 235 240	
acg gcg tat ggg ctg acg gtg ccc ccg ccg gtg atc gcc gag aac cgt	768
Thr Ala Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala Glu Asn Arg	
245 250 255	
gct gaa ctg atg att ctg ata gcg acc aac ctc ttg ggg caa aac acc	816
Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr	
260 265 270	

agt ggt gtg ctg cgt gtt ccg ccg cga ccc tat gtg atg ccg cat tct 1584
 Ser Gly Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met Pro His Ser
 515 520 525

ccg gca gcc ggc gat atc gcc ccg ccg gcc ttg tgg cag gac cgg ttc 1632
 Pro Ala Ala Gly Asp Ile Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe
 530 535 540

gcc gac ttc ccc gcg ctg ccc ctc gac ccg tcc gcg atg gtc gcc caa 1680
 Ala Asp Phe Pro Ala Leu Pro Leu Asp Pro Ser Ala Met Val Ala Gln
 545 550 555 560

gtg ggg cca cag gtg gtc aac atc aac acc aaa ctg ggc tac aac aac 1728
 Val Gly Pro Gln Val Val Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn
 565 570 575

gcc gtg ggc gcc ggg acc ggc atc gtc atc gat ccc aac ggt gtc gtg 1776
 Ala Val Gly Ala Gly Thr Gly Ile Val Ile Asp Pro Asn Gly Val Val
 580 585 590

ctg acc aac aac cac gtg atc gcg ggc gcc acc gac atc aat gcg ttc 1824
 Leu Thr Asn Asn His Val Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe
 595 600 605

agc gtc ggc tcc ggc caa acc tac ggc gtc gat gtg gtc ggg tat gac 1872
 Ser Val Gly Ser Gly Gln Thr Tyr Gly Val Asp Val Val Gly Tyr Asp
 610 615 620

cgc acc cag gat gtc gcg gtg ctg cag ctg cgc ggt gcc ggt ggc ctg 1920
 Arg Thr Gln Asp Val Ala Val Leu Gln Leu Arg Gly Ala Gly Gly Leu
 625 630 635 640

ccg tgg gcg gcg atc ggt ggc ggc gtc gcg gtt ggt gag ccc gtc gtc 1968
 Pro Ser Ala Ala Ile Gly Gly Gly Val Ala Val Gly Glu Pro Val Val
 645 650 655

gcg atg ggc aac agc ggt ggg cag ggc gga acg ccc cgt gcg gtg cct 2016
 Ala Met Gly Asn Ser Gly Gly Gln Gly Gly Thr Pro Arg Ala Val Pro
 660 665 670

ggc agg gtg gtc gcg ctc ggc caa acc gtg cag gcg tgg gat tgg ctg 2064
 Gly Arg Val Val Ala Leu Gly Gln Thr Val Gln Ala Ser Asp Ser Leu
 675 680 685

acc ggt gcc gaa gag aca ttg aac ggg ttg atc cag ttc gat gcc gcg 2112
 Thr Gly Ala Glu Glu Thr Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala
 690 695 700

atc cag ccc ggt gat tgg ggc ggg ccc gtc gtc aac ggc cta gga cag 2160
 Ile Gln Pro Gly Asp Ser Gly Gly Pro Val Val Asn Gly Leu Gly Gln
 705 710 715 720

gtg gtc ggt atg aac acg gcc gcg tcc tag g 2191
 Val Val Gly Met Asn Thr Ala Ala Ser
 725 730

<210> 12
 <211> 729
 <212> PRT
 <213> Artificial Sequence
 <223> Description of Artificial Sequence:Ra12-H9-32A fusion
 polypeptide (Ra12-MTB39-MTB32A(N-ter) fusion polypeptide)

<400> 12
 Met His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu
 1 5 10 15
 Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
 20 25 30
 Ile Ala Gly Gln Ile Arg Ser Gly Gly Gly Ser Pro Thr Val His Ile
 35 40 45
 Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn
 50 55 60
 Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu
 65 70 75 80
 Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile
 85 90 95
 Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly
 100 105 110
 Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr
 115 120 125
 Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala Glu Phe Met Val Asp
 130 135 140
 Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly
 145 150 155 160
 Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Gln Met Trp Asp Ser Val
 165 170 175
 Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser Val Val Trp
 180 185 190
 Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly Leu Met Val
 195 200 205
 Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr Ala Gly Gln
 210 215 220
 Ala Glu Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala Tyr Glu
 225 230 235 240
 Thr Ala Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala Glu Asn Arg
 245 250 255
 Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr
 260 265 270
 Pro Ala Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln
 275 280 285
 Asp Ala Ala Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr
 290 295 300
 Ala Thr Leu Leu Pro Phe Glu Glu Ala Pro Glu Met Thr Ser Ala Gly
 305 310 315 320
 Gly Leu Leu Glu Gln Ala Ala Ala Val Glu Glu Ala Ser Asp Thr Ala
 325 330 335
 Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu Gln Gln Leu
 340 345 350
 Ala Gln Pro Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu
 355 360 365
 Trp Lys Thr Val Ser Pro His Arg Ser Pro Ile Ser Asn Met Val Ser
 370 375 380
 Met Ala Asn Asn His Met Ser Met Thr Asn Ser Gly Val Ser Met Thr
 385 390 395 400
 Asn Thr Leu Ser Ser Met Leu Lys Gly Phe Ala Pro Ala Ala Ala Ala
 405 410 415

Gln Ala Val Gln Thr Ala Ala Gln Asn Gly Val Arg Ala Met Ser Ser
 420 425 430
 Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu Gly Gly Gly Val Ala Ala
 435 440 445
 Asn Leu Gly Arg Ala Ala Ser Val Gly Ser Leu Ser Val Pro Gln Ala
 450 455 460
 Trp Ala Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg Ala Leu Pro
 465 470 475 480
 Leu Thr Ser Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly Gln Met Leu
 485 490 495
 Gly Gly Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly Gly Gly Leu
 500 505 510
 Ser Gly Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met Pro His Ser
 515 520 525
 Pro Ala Ala Gly Asp Ile Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe
 530 535 540
 Ala Asp Phe Pro Ala Leu Pro Leu Asp Pro Ser Ala Met Val Ala Gln
 545 550 555 560
 Val Gly Pro Gln Val Val Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn
 565 570 575
 Ala Val Gly Ala Gly Thr Gly Ile Val Ile Asp Pro Asn Gly Val Val
 580 585 590
 Leu Thr Asn Asn His Val Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe
 595 600 605
 Ser Val Gly Ser Gly Gln Thr Tyr Gly Val Asp Val Val Gly Tyr Asp
 610 615 620
 Arg Thr Gln Asp Val Ala Val Leu Gln Leu Arg Gly Ala Gly Gly Leu
 625 630 635 640
 Pro Ser Ala Ala Ile Gly Gly Gly Val Ala Val Gly Glu Pro Val Val
 645 650 655
 Ala Met Gly Asn Ser Gly Gly Gln Gly Gly Thr Pro Arg Ala Val Pro
 660 665 670
 Gly Arg Val Val Ala Leu Gly Gln Thr Val Gln Ala Ser Asp Ser Leu
 675 680 685
 Thr Gly Ala Glu Glu Thr Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala
 690 695 700
 Ile Gln Pro Gly Asp Ser Gly Gly Pro Val Val Asn Gly Leu Gly Gln
 705 710 715 720
 Val Val Gly Met Asn Thr Ala Ala Ser
 725

<210> 13
 <211> 51
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:oligonucleotide
 primer for PCR amplification of Ral2 C-terminal
 fragment of MTB32A

<400> 13
 caattacata tgcataacca tcaccatcac acggccgcgt ccgataactt c

51

<210> 14
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:3'
oligonucleotide primer for PCR amplification of
Ral2 C-terminal fragment of MTB32A

<400> 14

ctaatacgaat tcggccgggg gtcctcggc caa

33

<210> 15

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:5'
oligonucleotide primer containing enterokinase
recognition site for PCR amplification of DPPD
mature secreted form

<400> 15

caattagaat tcgacgacga cgacaaggat ccacctgacc cgcacacag

48

<210> 16

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:3'
oligonucleotide primer containing enterokinase
recognition site for PCR amplification of DPPD
mature secreted form

<400> 16

caattagaat tctcagggag cgctgggctg etc

33

<210> 17

<211> 30

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Ral2(short)
polypeptide

<400> 17

Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe

1 5 10 15

Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile

20 25 30

<210> 18

<211> 128

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Ra12(long)
polypeptide

<400> 18

Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe
1 5 10 15
Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Lys Leu
20 25 30
Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val
35 40 45
Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala
50 55 60
Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val
65 70 75 80
Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn
85 90 95
Gly His His Pro Gly Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser
100 105 110
Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala
115 120 125

<210> 19

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:5'
oligonucleotide primer, HindIII site, for PCR
amplification of human mammaglobin

<400> 19

gcgaagctta tgaagttgct gatggtcttc atgc

34

<210> 20

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:3'
oligonucleotide primer, XhoI site, for PCR
amplification of human mammaglobin

<400> 20

cggtcgagt taaaataaat cacaaagact gctgtc

36

<210> 21

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Met-His tag 6aa

<400> 21
Met His His His His His His
1 5

<210> 22
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: enterokinase
recognition site

<400> 22
Asp Asp Asp Lys
1

Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Gly Pro Gln Val Val
 50 55 60
 Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly Thr
 65 70 75 80
 Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val
 85 90 95
 Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln
 100 105 110
 Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala
 115 120 125
 Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly
 130 135 140
 Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly
 145 150 155 160
 Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu
 165 170 175
 Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu Thr
 180 185 190
 Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser
 195 200 205
 Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn Thr
 210 215 220
 Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe Ala
 225 230 235 240
 Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser Gly
 245 250 255
 Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly Leu
 260 265 270
 Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val Val
 275 280 285
 Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val Ile
 290 295 300
 Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala Asp
 305 310 315 320
 Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Thr Trp Gln
 325 330 335
 Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu Gly
 340 345 350
 Pro Pro Ala
 355

<210> 3

<211> 396

<212> DNA

<213> Mycobacterium tuberculosis

<220>

<223> 14 KD C-terminal fragment of MTB32A Ra12

<220>

<221> CDS

<222> (1)..(396)

<223> Ra12

<400> 3

acg gcc gcg tcc gat aac ttc cag ctg tcc cag ggt ggg cag gga ttc
 Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe
 1 5 10 15

48

gcc att ccg atc ggg cag gcg atg gcg atc gcg ggc cag atc cga tcg 96
 Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser
 20 25 30

ggt ggg ggg tca ccc acc gtt cat atc ggg cct acc gcc ttc ctc ggc 144
 Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly
 35 40 45

ttg ggt gtt gtc gac aac aac ggc aac ggc gca cga gtc caa cgc gtg 192
 Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val
 50 55 60

gtc ggg agc gct ccg gcg gca agt ctc ggc atc tcc acc ggc gac gtg 240
 Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
 65 70 75 80

atc acc gcg gtc gac ggc gct ccg atc aac tcg gcc acc gcg atg gcg 288
 Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
 85 90 95

gac gcg ctt aac ggg cat cat ccc ggt gac gtc atc tcg gtg acc tgg 336
 Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Thr Trp
 100 105 110

caa acc aag tcg ggc ggc acg cgt aca ggg aac gtg aca ttg gcc gag 384
 Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu
 115 120 125

gga ccc ccg gcc 396
 Gly Pro Pro Ala
 130

<210> 4

<211> 132

<212> PRT

<213> Mycobacterium tuberculosis

<220>

<223> 14 KD C-terminal fragment of MTB32A Ra12

<400> 4

Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe
 1 5 10 15
 Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser
 20 25 30
 Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly
 35 40 45
 Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val
 50 55 60
 Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
 65 70 75 80
 Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
 85 90 95
 Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Thr Trp
 100 105 110
 Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu
 115 120 125
 Gly Pro Pro Ala
 130

<400> 17
 Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe
 1 5 10 15
 Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile
 20 25 30

<210> 18
 <211> 128
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Ra12(long)
 polypeptide

full-length

<400> 18
 Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe
 1 5 10 15
 Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Lys Leu
 20 25 30
 Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val
 35 40 45
 Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala
 50 55 60
 Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val
 65 70 75 80
 Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn
 85 90 95
 Gly His His Pro Gly Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser
 100 105 110
 Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala
 115 120 125

<210> 19
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:5'
 oligonucleotide primer, HindIII site, for PCR
 amplification of human mammaglobin

<400> 19
 gcgaagctta tgaagttgct gatggtcctc atgc

34

<210> 20
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:3'
 oligonucleotide primer, XhoI site, for PCR
 amplification of human mammaglobin

<400> 20
 cggctcgagt taaaataaat cacaaagact gctgtc

36

<210> 21
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Met-His tag 6aa

<400> 21
 Met His His His His His His
 1 5

<210> 22
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:enterokinase
 recognition site

<400> 22
 Asp Asp Asp Lys
 1

<210> 23
 <211> 128
 <212> PRT
 <213> Mycobacterium tuberculosis

<220>
 <223> positions 1-128 of Ra12

<400> 23
 Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe
 1 5 10 15
 Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser
 20 25 30
 Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly
 35 40 45
 Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val
 50 55 60
 Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
 65 70 75 80
 Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
 85 90 95
 Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Thr Trp
 100 105 110
 Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu ← NO:4 + Gly P. Pro Ala
 115 120 125